OIPE

RAW SEQUENCE LISTING   DATE: 09/21/2001
PATENT APPLICATION: US/09/943,692   TIME: 18:02:38

Input Set : **A:\Mobt195.ST25.txt**
Output Set: **N:\CRF3\09212001\I943692.raw**

```
 3 <110> APPLICANT: FISCHHOFF, DAVID A.
 4       FUCHS, ROY L.
 5       LAVRIK, PAUL B.
 6       McPHERSON, SYLVIA A.
 7       PERLAK, FREDERICK J.
 9 <120> TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
11 <130> FILE REFERENCE: MOBT:195--1
13 <140> CURRENT APPLICATION NUMBER: US/09/943,692
13 <141> CURRENT FILING DATE: 2001-08-31
13 <150> PRIOR APPLICATION NUMBER: 09/027,998
14 <151> PRIOR FILING DATE: 1998-02-23
16 <160> NUMBER OF SEQ ID NOS: 54
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2615
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Chimeric toxin gene
29 <400> SEQUENCE: 1
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32 tgtataaatt atttatcttg aaaggaggga tgcctaaaaa cgaagaacat taaaaacata   120
34 tatttgcacc gtctaatgga tttatgaaaa atcattttat cagtttgaaa attatgtatt   180
36 atgataagaa agggaggaag aaaaatgaat ccgaacaatc gaagtgaaca tgatacaata   240
38 aaaactactg aaaataatga ggtgccaact aaccatgttc aatatccttt agcggaaact   300
40 ccaaatccaa cactagaaga tttaaattat aaagagtttt taagaatgac tgcagataat   360
42 aatacggaag cactagatag ctctacaaca aaagatgtca ttcaaaaagg catttccgta   420
44 gtaggtgatc tcctaggcgt agtaggtttc ccgtttggtg gagcgcttgt ttcgttttat   480
46 acaaactttt aaatactat ttggccaagt gaagaccgt ggaaggcttt tatggaacaa     540
48 gtagaagcat tgatggatca gaaaatagct gattatgcaa aaaataaagc tcttgcagag   600
50 ttacagggcc ttcaaaataa tgtcgaagat tatgtgagtg cattgagttc atggcaaaaa   660
52 aatcctgtga gttcacgaaa tccacatagc caggggcgga taagagagct gttttctcaa   720
54 gcagaaagtc attttcgtaa ttcaatgcct tcgtttgcaa tttctggata cgaggttcta   780
56 tttctaacaa catatgcaca agctgccaac acacatttat ttttactaaa agacgctcaa   840
58 atttatggag aagaatgggg atacgaaaaa gaagatattg ctgaatttta taaaagacaa   900
60 ctaaaactta cgcaagaata tactgaccat tgtgtcaaat ggtataatgt tggattagat   960
62 aaattaagag gttcatctta tgaatcttgg gtaaacttta accgttatcg cagagagatg   1020
64 acattaacag tattagattt aattgcacta tttccattgt atgatgttcg gctataccca   1080
66 aaagaagtta aaccgaatt aacaagagac gttttaacag atccaattgt cggagtcaac   1140
68 aaccttaggg gctatggaac aaccttctct aatatagaaa attatattcg aaaaccacat   1200
70 ctatttgact atctgcatag aattcaattt cacacgcggt tccaaccagg atattatgga   1260
72 aatgactctt tcaattattg gtccggtaat tatgtttcaa ctagaccaag cataggatca   1320
74 aatgatataa tcacatctcc attctatgga aataaatcca gtgaacctgt acaaaattta   1380
76 gaatttaatg gagaaaaagt ctatagagcc gtagcaaata caatcttgc ggtctggccg   1440
78 tccgctgtat attcaggtgt tacaaaagtg gaatttagcc aatataatga tcaaacagat   1500
80 gaagcaagta cacaaacgta cgactcaaaa agaaatgttg gcgcggtcag ctgggattct   1560
82 atcgatcaat tgcctccaga aacaacagat gaacctctag aaaagggata tagccatcaa   1620
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Input Set : A:\Mobtl95.ST25.txt
Output Set: N:\CRF3\09212001\I943692.raw

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84  ctcaattatg taatgtgctt tttaatgcag ggtagtagag gaacaatccc agtgttaact  1680
86  tggacacata aaagtgtaga cttttttaac atgattgatt cgaaaaaaat tacacaactt  1740
88  ccgttagtaa aggcatataa gttacaatct ggtgcttccg ttgtcgcagg tcctaggttt  1800
90  acaggaggag atatcattca atgcacagaa aatggaagtg cggcaactat ttacgttaca  1860
92  ccggatgtgt cgtactctca aaaatatcga gctagaattc attatgcttc tacatctcag  1920
94  ataacattta cactcagttt agacggggca ccatttaatc aatactattt cgataaaacg  1980
96  ataaataaag gagacacatt aacgtataat tcatttaatt tagcaagttt cagcacacca  2040
98  ttcgaattat cagggaataa cttacaaata ggcgtcacag gattaagtgc tggagataaa  2100
100 gtttatatag acaaaattga atttattcca gtgaattaaa ttaactagaa agtaaagaag  2160
102 tagtgaccat ctatgatagt aagcaaagga taaaaaaatg agttcataaa atgaataaca  2220
104 tagtgttctt caactttcgc tttttgaagg tagatgaaga acactatttt tattttcaaa  2280
106 atgaaggaag tttttaaatat gtaatcattt aaagggaaca atgaaagtag gaaataagtc  2340
108 attatctata acaaaataac cattttata tagccagaaa tgaattataa tattaatctt  2400
110 ttctaaattg acgtttttct aaacgttcta tagcttcaag acgcttagaa tcatcaatat  2460
112 ttgtatacag agctgttgtt tccatcgagt tatgtcccat ttgattcgct aatagaacaa  2520
114 gatctttatt ttcgttataa tgattggttg cataagtatg gcgtaattta tgagggcttt  2580
116 tcttttcatc caaaagccaa gtgtatttct ctgta                             2615
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119 <210> SEQ ID NO: 2
120 <211> LENGTH: 644
121 <212> TYPE: PRT
122 <213> ORGANISM: Artificial Sequence
124 <220> FEATURE:
125 <223> OTHER INFORMATION: Chimeric toxin
128 <400> SEQUENCE: 2

```
130 Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Thr Thr Glu
131 1               5                   10              15
134 Asn Asn Glu Val Pro Thr Asn His Val Gln Tyr Pro Leu Ala Glu Thr
135             20                  25                  30
138 Pro Asn Pro Thr Leu Glu Asp Leu Asn Tyr Lys Glu Phe Leu Arg Met
139         35                  40                  45
142 Thr Ala Asp Asn Asn Thr Glu Ala Leu Asp Ser Ser Thr Thr Lys Asp
143     50                  55                  60
146 Val Ile Gln Lys Gly Ile Ser Val Val Gly Asp Leu Leu Gly Val Val
147 65                  70                  75                  80
150 Gly Phe Pro Phe Gly Gly Ala Leu Val Ser Phe Tyr Thr Asn Phe Leu
151                 85                  90                  95
154 Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Glu Gln
155             100                 105                 110
158 Val Glu Ala Leu Met Asp Gln Lys Ile Ala Asp Tyr Ala Lys Asn Lys
159             115                 120                 125
162 Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Val Glu Asp Tyr Val
163     130                 135                 140
166 Ser Ala Leu Ser Ser Trp Gln Lys Asn Pro Val Ser Ser Arg Asn Pro
167 145                 150                 155                 160
170 His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His
171                 165                 170                 175
174 Phe Arg Asn Ser Met Pro Ser Phe Ala Ile Ser Gly Tyr Glu Val Leu
175             180                 185                 190
178 Phe Leu Thr Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Phe Leu Leu
```

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Input Set : A:\Mobt195.ST25.txt
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```
179          195                200                205
182 Lys Asp Ala Gln Ile Tyr Gly Glu Glu Trp Gly Tyr Glu Lys Glu Asp
183      210                215                220
186 Ile Ala Glu Phe Tyr Lys Arg Gln Leu Lys Leu Thr Gln Glu Tyr Thr
187 225                230                235                240
190 Asp His Cys Val Lys Trp Tyr Asn Val Gly Leu Asp Lys Leu Arg Gly
191              245                250                255
194 Ser Ser Tyr Glu Ser Trp Val Asn Phe Asn Arg Tyr Arg Arg Glu Met
195          260                265                270
198 Thr Leu Thr Val Leu Asp Leu Ile Ala Leu Phe Pro Leu Tyr Asp Val
199      275                280                285
202 Arg Leu Tyr Pro Lys Glu Val Lys Thr Glu Leu Thr Arg Asp Val Leu
203      290                295                300
206 Thr Asp Pro Ile Val Gly Val Asn Asn Leu Arg Gly Tyr Gly Thr Thr
207 305              310                315                320
210 Phe Ser Asn Ile Glu Asn Tyr Ile Arg Lys Pro His Leu Phe Asp Tyr
211              325                330                335
214 Leu His Arg Ile Gln Phe His Thr Arg Phe Gln Pro Gly Tyr Tyr Gly
215          340                345                350
218 Asn Asp Ser Phe Asn Tyr Trp Ser Gly Asn Tyr Val Ser Thr Arg Pro
219          355                360                365
222 Ser Ile Gly Ser Asn Asp Ile Ile Thr Ser Pro Phe Tyr Gly Asn Lys
223      370                375                380
226 Ser Ser Glu Pro Val Gln Asn Leu Glu Phe Asn Gly Glu Lys Val Tyr
227 385              390                395                400
230 Arg Ala Val Ala Asn Thr Asn Leu Ala Val Trp Pro Ser Ala Val Tyr
231              405                410                415
234 Ser Gly Val Thr Lys Val Glu Phe Ser Gln Tyr Asn Asp Gln Thr Asp
235          420                425                430
238 Glu Ala Ser Thr Gln Thr Tyr Asp Ser Lys Arg Asn Val Gly Ala Val
239      435                440                445
242 Ser Trp Asp Ser Ile Asp Gln Leu Pro Pro Glu Thr Thr Asp Glu Pro
243 450                455                460
246 Leu Glu Lys Gly Tyr Ser His Gln Leu Asn Tyr Val Met Cys Phe Leu
247 465                470                475                480
250 Met Gln Gly Ser Arg Gly Thr Ile Pro Val Leu Thr Trp Thr His Lys
251          485                490                495
254 Ser Val Asp Phe Phe Asn Met Ile Asp Ser Lys Lys Ile Thr Gln Leu
255          500                505                510
258 Pro Leu Val Lys Ala Tyr Lys Leu Gln Ser Gly Ala Ser Val Val Ala
259      515                520                525
262 Gly Pro Arg Phe Thr Gly Gly Asp Ile Ile Gln Cys Thr Glu Asn Gly
263      530                535                540
266 Ser Ala Ala Thr Ile Tyr Val Thr Pro Asp Val Ser Tyr Ser Gln Lys
267 545                550                555                560
270 Tyr Arg Ala Arg Ile His Tyr Ala Ser Thr Ser Gln Ile Thr Phe Thr
271          565                570                575
274 Leu Ser Leu Asp Gly Ala Pro Phe Asn Gln Tyr Tyr Phe Asp Lys Thr
275          580                585                590
```

```
278 Ile Asn Lys Gly Asp Thr Leu Thr Tyr Asn Ser Phe Asn Leu Ala Ser
279         595             600             605
282 Phe Ser Thr Pro Phe Glu Leu Ser Gly Asn Asn Leu Gln Ile Gly Val
283     610             615             620
286 Thr Gly Leu Ser Ala Gly Asp Lys Val Tyr Ile Asp Lys Ile Glu Phe
287 625             630             635             640
290 Ile Pro Val Asn
294 <210> SEQ ID NO: 3
295 <211> LENGTH: 15
296 <212> TYPE: PRT
297 <213> ORGANISM: Bacillus thuringiensis
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W--> 298 **<400> SEQUENCE: 3**

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300 Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Thr Thr
301 1           5               10              15
304 <210> SEQ ID NO: 4
305 <211> LENGTH: 45
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: Synthetic Oligonucleotide
312 <220> FEATURE:
313 <221> NAME/KEY: misc_feature
314 <222> LOCATION: (9)..(9)
315 <223> OTHER INFORMATION: N = A, C, G or T
319 <220> FEATURE:
320 <221> NAME/KEY: misc_feature
321 <222> LOCATION: (18)..(18)
322 <223> OTHER INFORMATION: N = A, C, G or T
326 <220> FEATURE:
327 <221> NAME/KEY: misc_feature
328 <222> LOCATION: (21)..(21)
329 <223> OTHER INFORMATION: N = A, C, G or T
333 <220> FEATURE:
334 <221> NAME/KEY: misc_feature
335 <222> LOCATION: (33)..(33)
336 <223> OTHER INFORMATION: N = A, C, G or T
340 <220> FEATURE:
341 <221> NAME/KEY: misc_feature
342 <222> LOCATION: (42)..(42)
343 <223> OTHER INFORMATION: N = A, C, G or T
347 <220> FEATURE:
348 <221> NAME/KEY: misc_feature
349 <222> LOCATION: (45)..(45)
350 <223> OTHER INFORMATION: N = A, C, G or T
353 <400> SEQUENCE: 4
354 atgaatccna ataatcgntc ngaacatgat acnattaaaa cnacn          45
357 <210> SEQ ID NO: 5
358 <211> LENGTH: 45
359 <212> TYPE: DNA
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Input Set : A:\Mobt195.ST25.txt
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360 <213> ORGANISM: Artificial Sequence
362 <220> FEATURE:
363 <223> OTHER INFORMATION: Synthetic Oligonucleotide
365 <220> FEATURE:
366 <221> NAME/KEY: misc_feature
367 <222> LOCATION: (9)..(9)
368 <223> OTHER INFORMATION: N = A, C, G or T
372 <220> FEATURE:
373 <221> NAME/KEY: misc_feature
374 <222> LOCATION: (33)..(33)
375 <223> OTHER INFORMATION: N = A, C, G or T
379 <220> FEATURE:
380 <221> NAME/KEY: misc_feature
381 <222> LOCATION: (42)..(42)
382 <223> OTHER INFORMATION: N = A, C, G or T
386 <220> FEATURE:
387 <221> NAME/KEY: misc_feature
388 <222> LOCATION: (45)..(45)
389 <223> OTHER INFORMATION: N = A, C, G or T
392 <400> SEQUENCE: 5
393 atgaacccna acaacagaag tgagcacgac acnatcaaga cnacn                45
396 <210> SEQ ID NO: 6
397 <211> LENGTH: 45
398 <212> TYPE: DNA
399 <213> ORGANISM: Artificial Sequence
401 <220> FEATURE:
402 <223> OTHER INFORMATION: Synthetic Oligonucleotide
404 <220> FEATURE:
405 <221> NAME/KEY: misc_feature
406 <222> LOCATION: (9)..(9)
407 <223> OTHER INFORMATION: N = A, C, G or T
411 <220> FEATURE:
412 <221> NAME/KEY: misc_feature
413 <222> LOCATION: (33)..(33)
414 <223> OTHER INFORMATION: N = A, C, G or T
418 <220> FEATURE:
419 <221> NAME/KEY: misc_feature
420 <222> LOCATION: (42)..(42)
421 <223> OTHER INFORMATION: N = A, C, G or T
425 <220> FEATURE:
426 <221> NAME/KEY: misc_feature
427 <222> LOCATION: (45)..(45)
428 <223> OTHER INFORMATION: N = A, C, G or T
431 <400> SEQUENCE: 6
432 atgaatccna ataatcggtc cgaacatgat acnataaaaa cnacn                45
435 <210> SEQ ID NO: 7
436 <211> LENGTH: 17
437 <212> TYPE: DNA
438 <213> ORGANISM: Artificial Sequence
```

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/943,692

DATE: 09/21/2001
TIME: 18:02:39

Input Set : **A:\Mobt195.ST25.txt**
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```
L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:298 M:283 W: Missing Blank Line separator, <400> field identifier
L:354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:393 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:903 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:986 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1117 M:283 W: Missing Blank Line separator, <400> field identifier
L:1125 M:283 W: Missing Blank Line separator, <400> field identifier
L:1148 M:283 W: Missing Blank Line separator, <400> field identifier
L:1156 M:283 W: Missing Blank Line separator, <400> field identifier
L:1179 M:283 W: Missing Blank Line separator, <400> field identifier
L:1187 M:283 W: Missing Blank Line separator, <400> field identifier
L:1212 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:1215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:54
L:1215 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:1218 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:54
L:1218 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
```